

F. Moezie

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1653

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/068,253

DATE: 04/20/2001  
TIME: 12:57:28

Input Set : A:\19624051.app  
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3 <110> APPLICANT: SHIMURA, Takesada  
4 TORIYAMA, Satsuki  
6 <120> TITLE OF INVENTION: CARTILAGE/ BONE INDUCING MATERIALS FOR REPARATION  
8 <130> FILE REFERENCE: 146.1286  
10 <140> CURRENT APPLICATION NUMBER: 09/068,253  
11 <141> CURRENT FILING DATE: 1998-06-09  
13 <150> PRIOR APPLICATION NUMBER: PCT/JP96/03333  
14 <151> PRIOR FILING DATE: 1996-11-14  
16 <150> PRIOR APPLICATION NUMBER: JP 7/322402  
17 <151> PRIOR FILING DATE: 1995-11-17  
19 <160> NUMBER OF SEQ ID NOS: 4  
21 <170> SOFTWARE: PatentIn Ver. 2.1  
23 <210> SEQ ID NO: 1  
24 <211> LENGTH: 357  
25 <212> TYPE: DNA  
26 <213> ORGANISM: Homo sapiens  
28 <220> FEATURE:  
29 <221> NAME/KEY: CDS  
30 <222> LOCATION: (1)..(357)  
31 <223> OTHER INFORMATION: Relevant amino acid residues in SEQ ID NO: 1 from  
32 1 to 119 in WO 95/04819  
34 <300> PUBLICATION INFORMATION:  
35 <301> AUTHORS: HOTTEN, Gertrud  
36 NEIDHARDT, Helge  
37 PAULISTA, Michael  
38 <302> TITLE: NEW GROWTH/DIFFERENTIATION FACTOR OF THE TGF-BETA  
39 FAMILY  
40 <310> PATENT DOC NO: WO 95/04819  
41 <311> PATENT FILING DATE: 1995-02-16  
42 <313> RELEVANT RESIDUES: 1 TO 119  
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46 Pro Leu Ala Thr Arg Gln Gly Lys Arg Pro Ser Lys Asn Leu Lys Ala  
47 1 5 10 15  
49 cgc tgc agt cgg aag gca ctg cat gtc aac ttc aag gac atg ggc tgg 96  
50 Arg Cys Ser Arg Lys Ala Leu His Val Asn Phe Lys Asp Met Gly Trp  
51 20 25 30  
53 gac gac tgg atc atc gca ccc ctt gag tac gag gct ttc cac tgc gag 144  
54 Asp Asp Trp Ile Ile Ala Pro Leu Glu Tyr Glu Ala Phe His Cys Glu  
55 35 40 45  
57 ggg ctg tgc gag ttc cca ttg cgc tcc cac ctg gag ccc acg aat cat 192  
58 Gly Leu Cys Glu Phe Pro Leu Arg Ser His Leu Glu Pro Thr Asn His  
59 50 55 60  
61 gca gtc atc cag acc ctg atg aac tcc atg gac ccc gag tcc aca cca 240  
62 Ala Val Ile Gln Thr Leu Met Asn Ser Met Asp Pro Glu Ser Thr Pro  
63 65 70 75 80  
65 ccc acc tgc tgt gtg ccc acg cga ctg agt ccc atc agc atc ctc ttc 288

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66 Pro Thr Cys Cys Val Pro Thr Arg Leu Ser Pro Ile Ser Ile Leu Phe
67      85      90      95
69 att gac tct gcc aac aac gtg gtg tat aag cag tat gag gac atg gtc 336
70 Ile Asp Ser Ala Asn Asn Val Val Tyr Lys Gln Tyr Glu Asp Met Val
71      100      105      110
73 gtg gag tcg tgt gcc tgc agg 357
74 Val Glu Ser Cys Gly Cys Arg
75      115
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80 <212> TYPE: PRT
81 <213> ORGANISM: Homo sapiens
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87 Arg Cys Ser Arg Lys Ala Leu His Val Asn Phe Lys Asp Met Gly Trp
88      20      25      30
90 Asp Asp Trp Ile Ile Ala Pro Leu Glu Tyr Glu Ala Phe His Cys Glu
91      35      40      45
93 Gly Leu Cys Glu Phe Pro Leu Arg Ser His Leu Glu Pro Thr Asn His
94      50      55      60
96 Ala Val Ile Gln Thr Leu Met Asn Ser Met Asp Pro Glu Ser Thr Pro
97      65      70      75      80
99 Pro Thr Cys Cys Val Pro Thr Arg Leu Ser Pro Ile Ser Ile Leu Phe
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102 Ile Asp Ser Ala Asn Asn Val Val Tyr Lys Gln Tyr Glu Asp Met Val
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106      115
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122 <223> OTHER INFORMATION: PCR forward primer for isolating mature-type MP52
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125 ataatgccac tagcaactcg tcagggc 27
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131 <213> ORGANISM: Artificial Sequence
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140 <223> OTHER INFORMATION: PCR reverse primer for isolating mature-type MP52  
142 <400> SEQUENCE: 4  
143 cgtcgactac ctgcagccac acgact . 26

VERIFICATION SUMMARY

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